

1/20

Band 55 protein

	10	20	30	40	50
ISR	MESAEELPARPALETEGLRFLHVTVGSLASYGWYVLFSCILLYIVIQK				
MOUSE	-DRD----S-@-----S-*-----I-----R				
RAT	---S-----S-----I---V-----				
HUMAN	--RQ--S-S-----T-----T---IV-----V-F--				
	60	70	80	90	100
ISR	LSVRLRALRQRQLDQADAVLEPDVVKRQEALAAARLRMQEDLNAQVEKH				
MOUSE	--L-----ET---V-----				
RAT	--L-----E---V-----				
HUMAN	--A-----R-A-AV---V-----K---E-----				
	110	120	130	140	150
ISR	KEKLRQLEEEKRRQKIEMWDSMQEGRSYRRNPGRPQEEDGPGPSTSSSVT				
MOUSE	-----K--S-----/--I				
RAT	-----K-----/--I				
HUMAN	----K-----K-KG-AKK----S-----/--L				
	160	170	180	189	
ISR	RKGKSDKKPLRGNGYNPLTGEGGGTCAWRPGRRGPSGG				
MOUSE	P-----G-----S-----				
RAT	P-----G-----				
HUMAN	/-R--R---G-----S-----A-S-----				

@=R or S

*=R or Q

A= mixture of A and V

Figure 1

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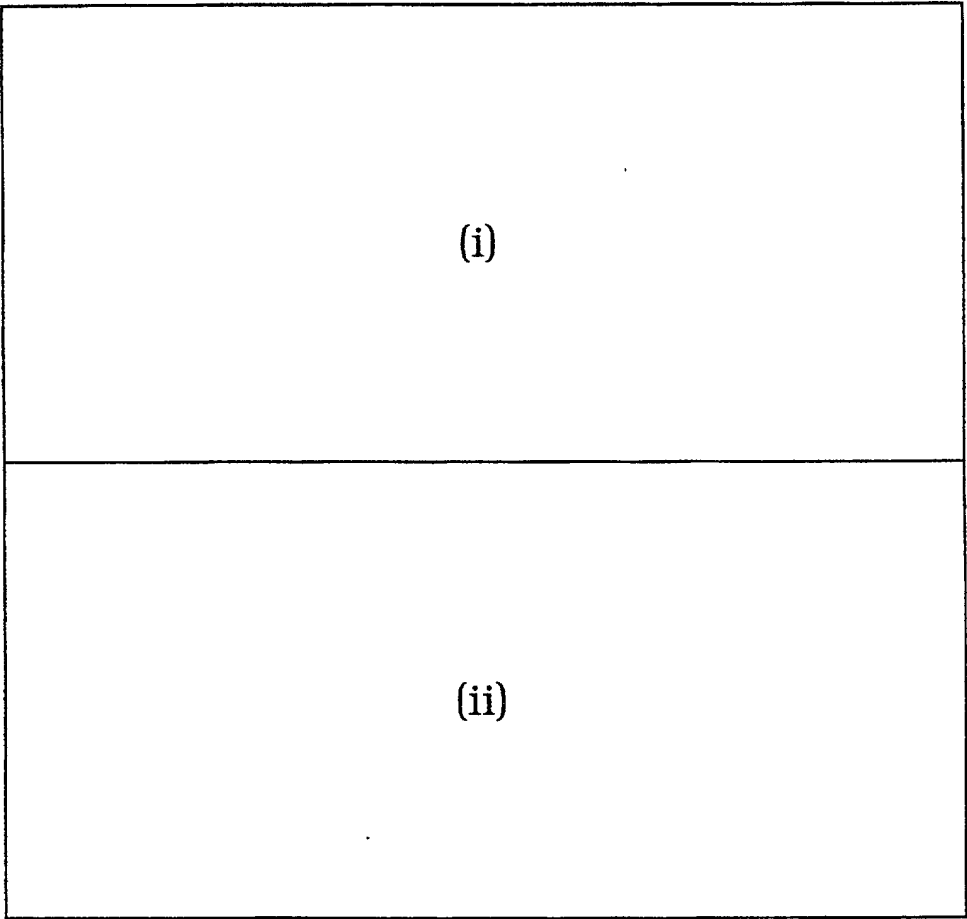


Figure 2

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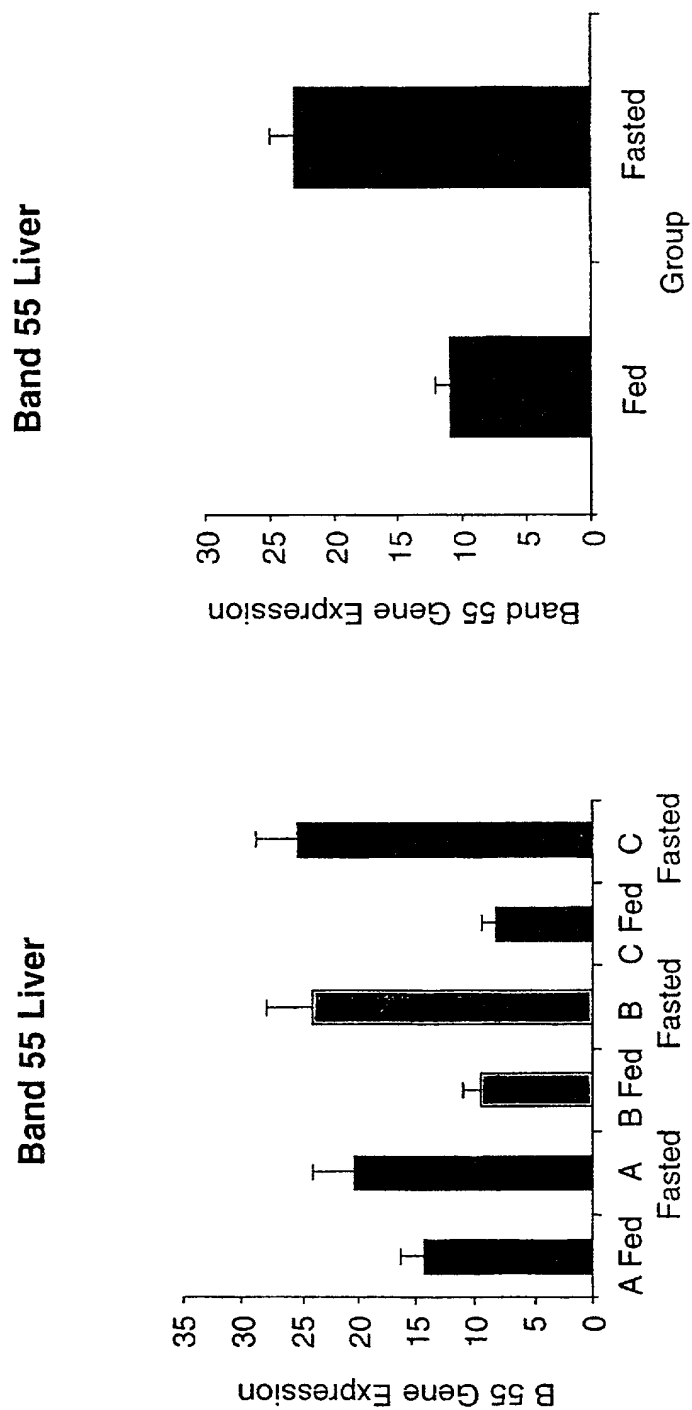


Figure 2(i)

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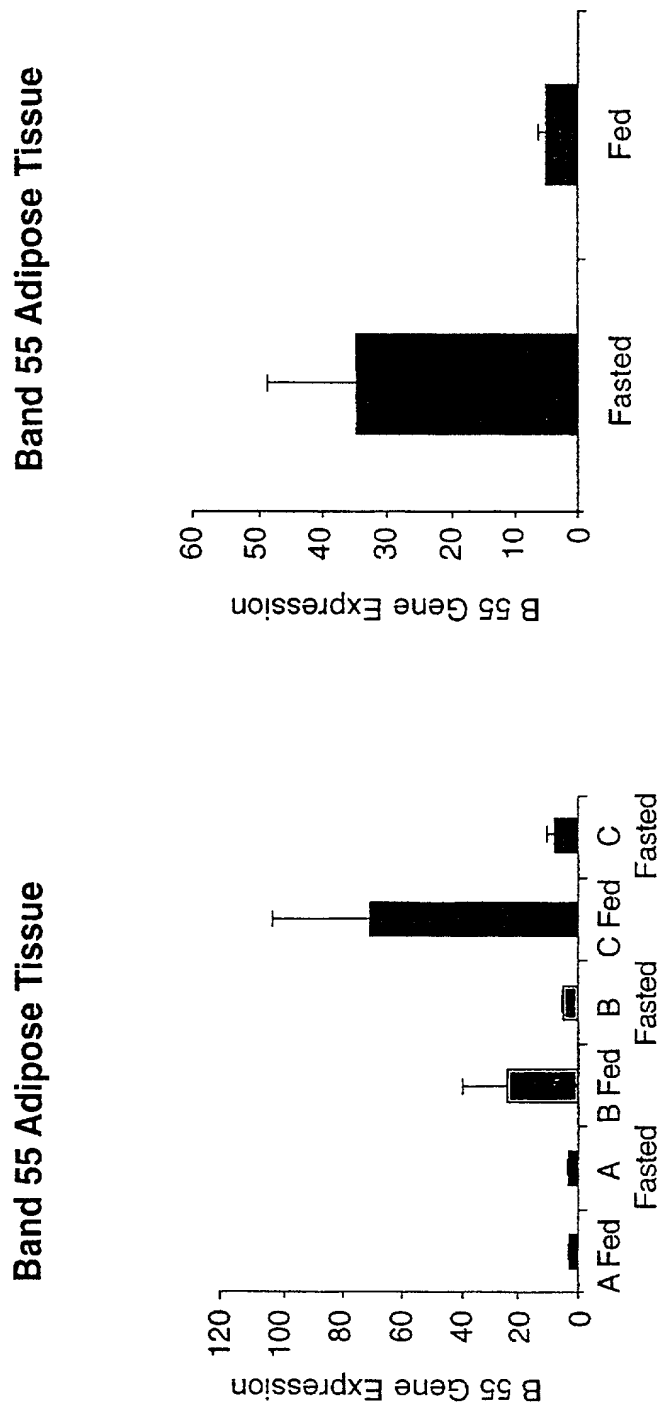


Figure 2(ii)

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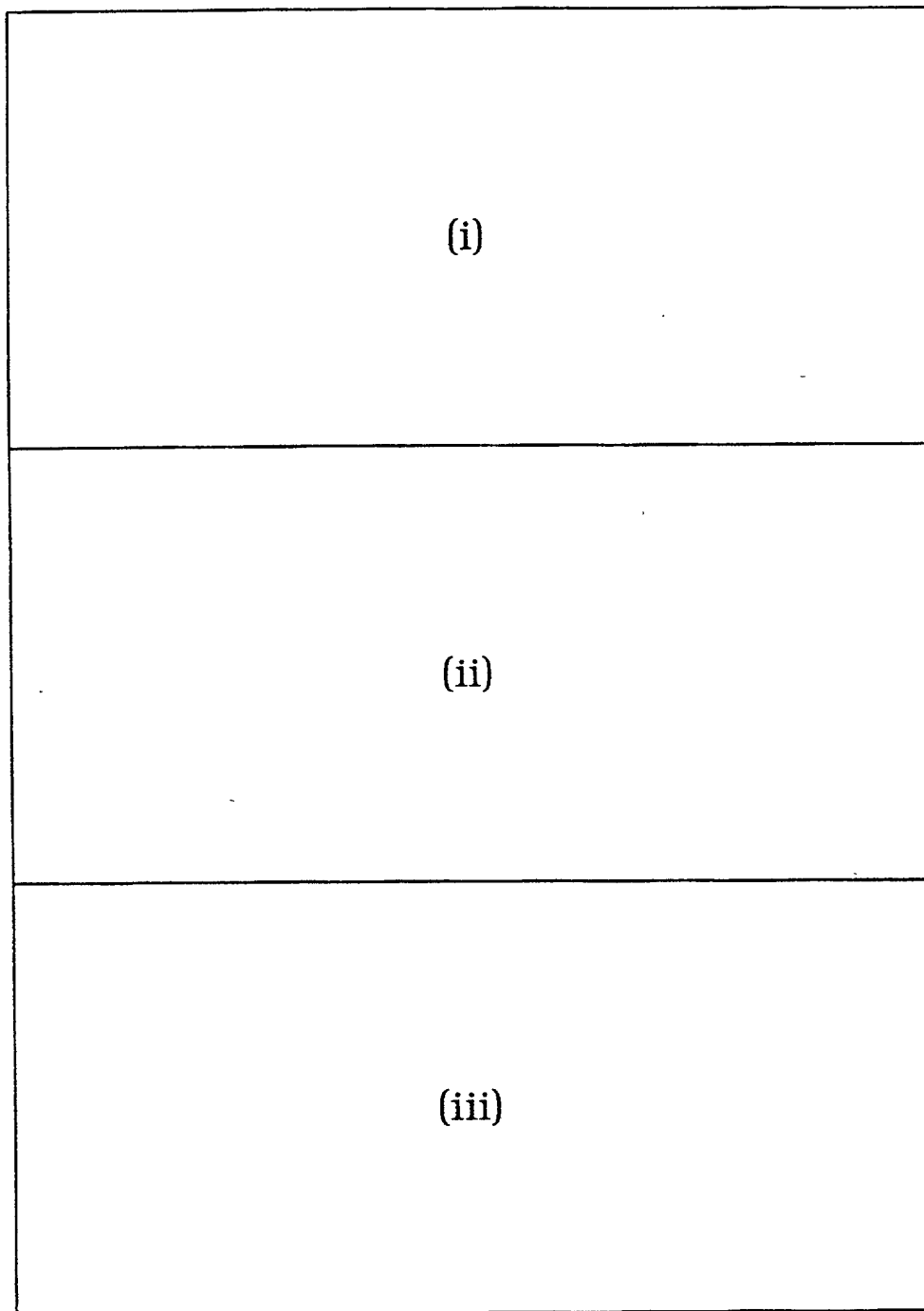


Figure 3

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Band 60 v. Body Weight - All animals Band 60 v. Body Weight - A animals

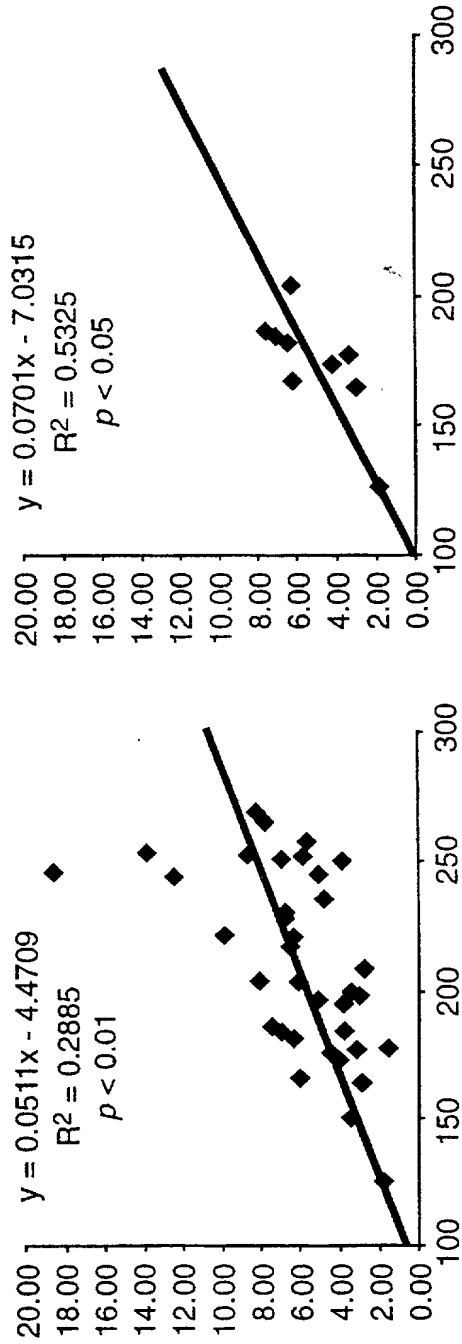


Figure 3(i)

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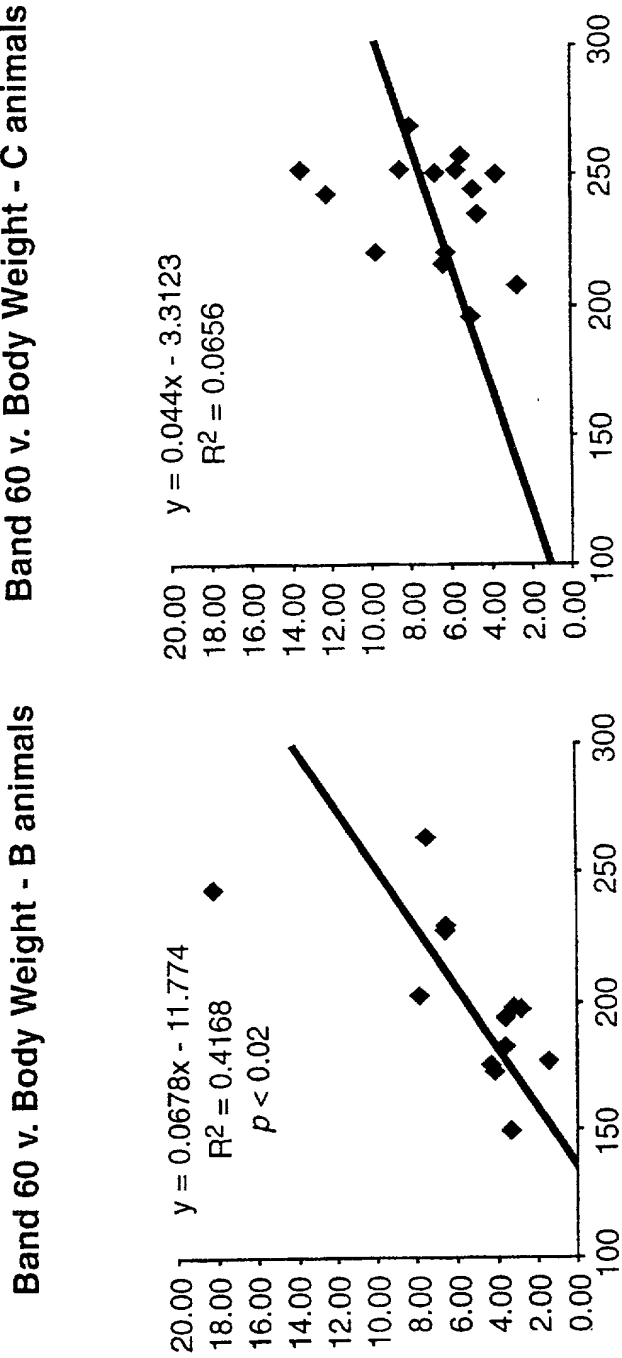


Figure 3(ii)

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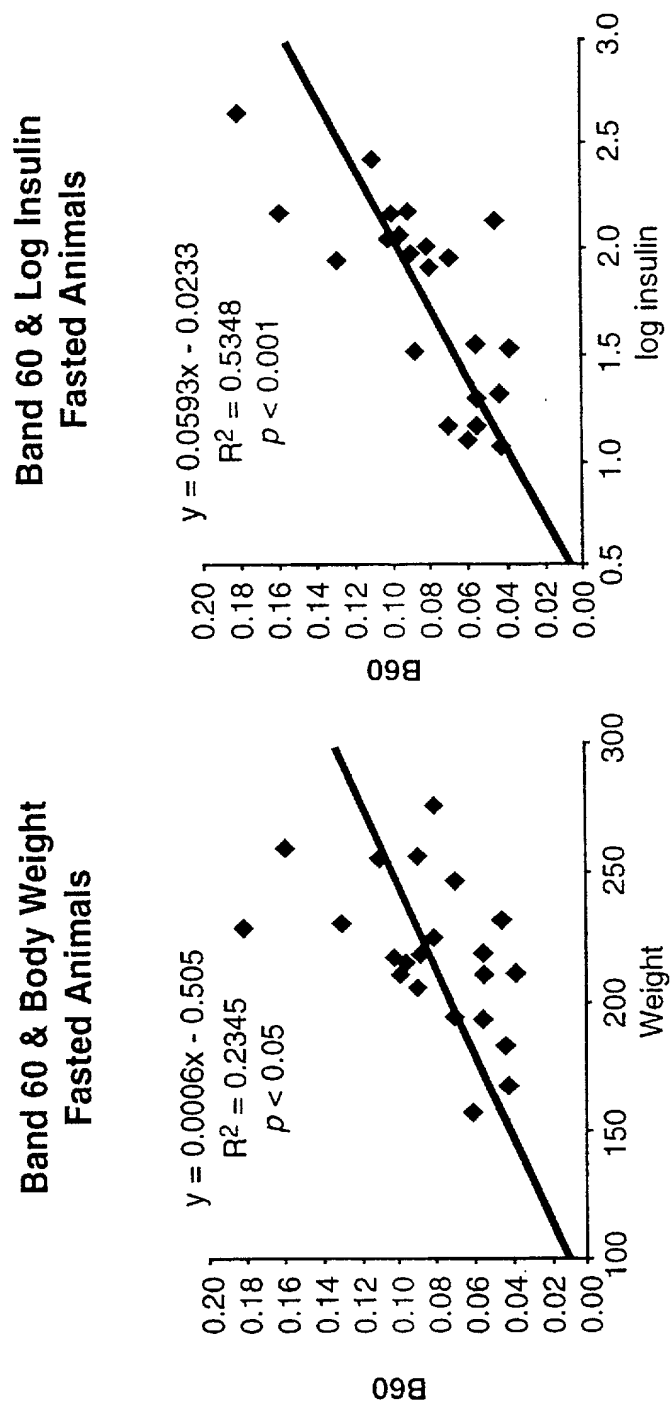


Figure 3(iii)

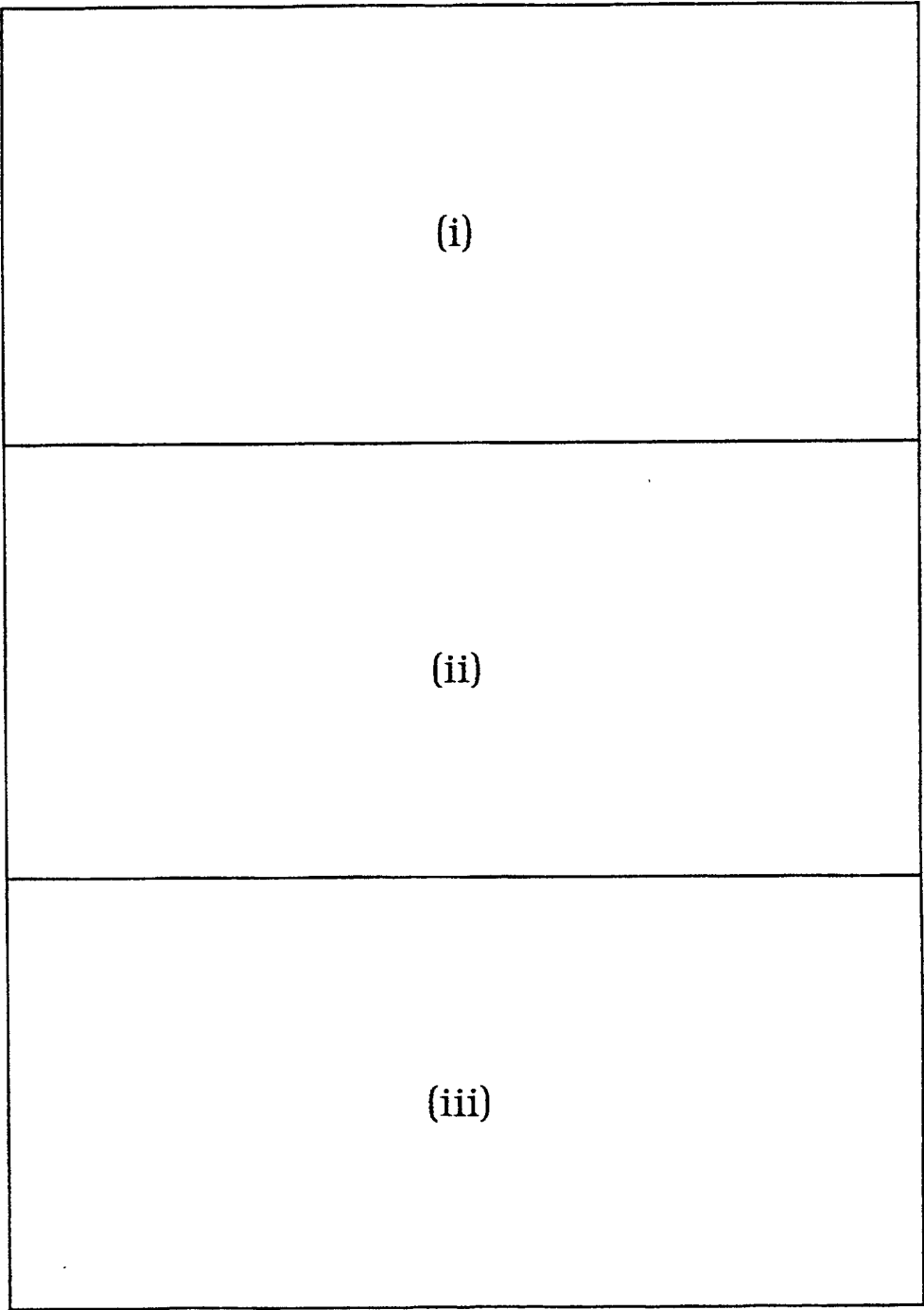
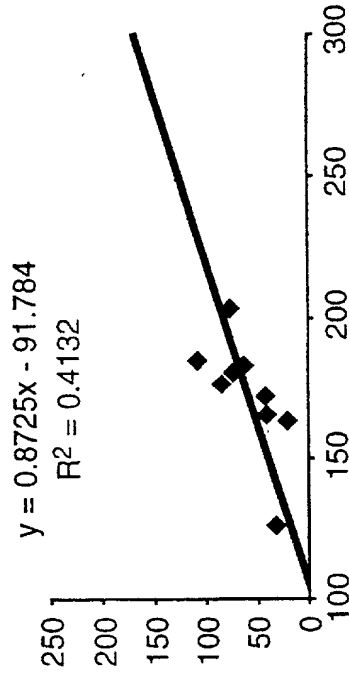


Figure 4

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LIVER

Band 38 v. Body weight - A animals



Band 38 v. Body weight - All animals

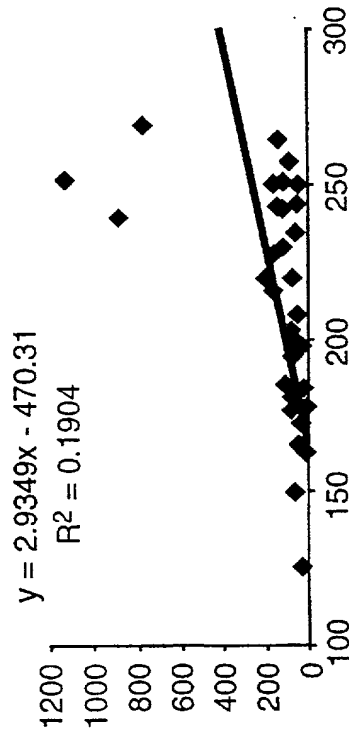
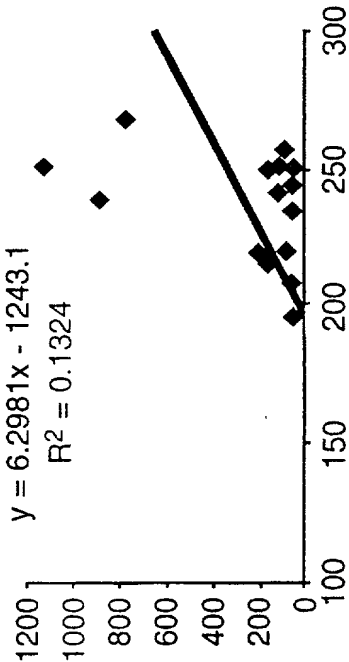


Figure 4(i)

Band 38 v. Body weight - C animals



Band 38 v. Body weight - B animals

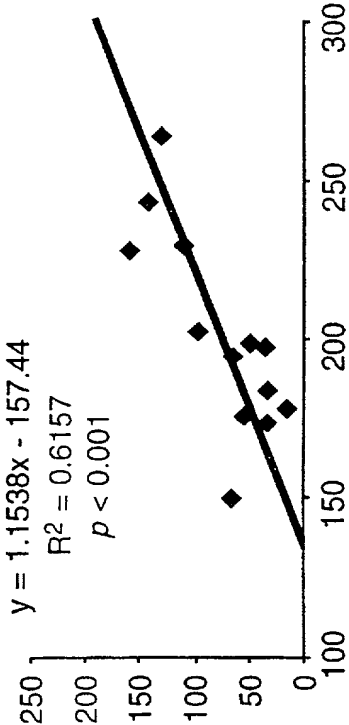
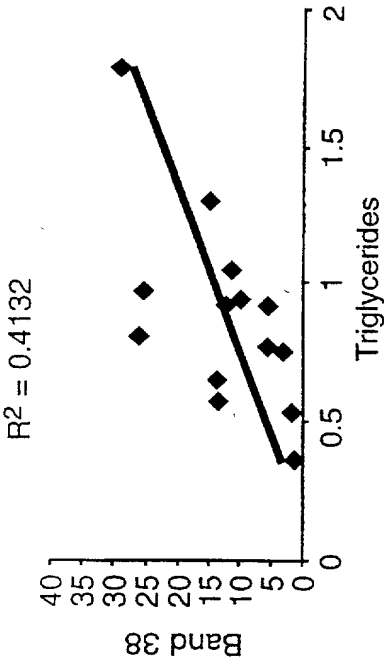


Figure 4(ii)

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Adipose tissue - Band 38 v triglycerides



Liver - Band 38 v. Triglycerides

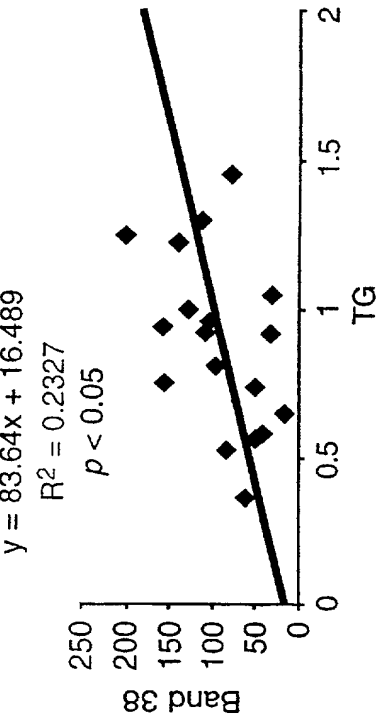


Figure 4(iii)

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Genomic structure of the human band 55 gene

Chromosome 15

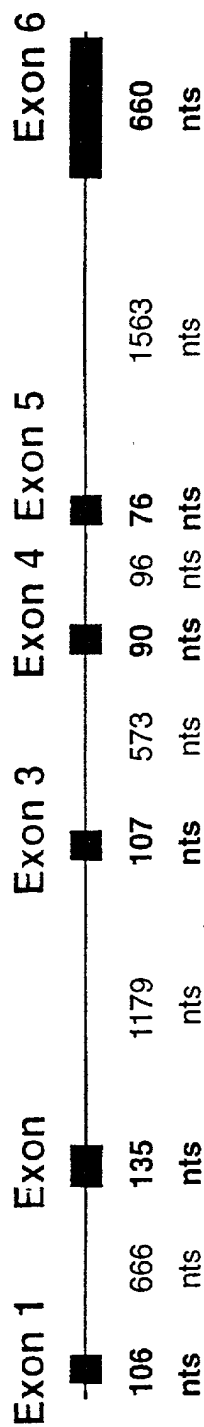


Figure 5

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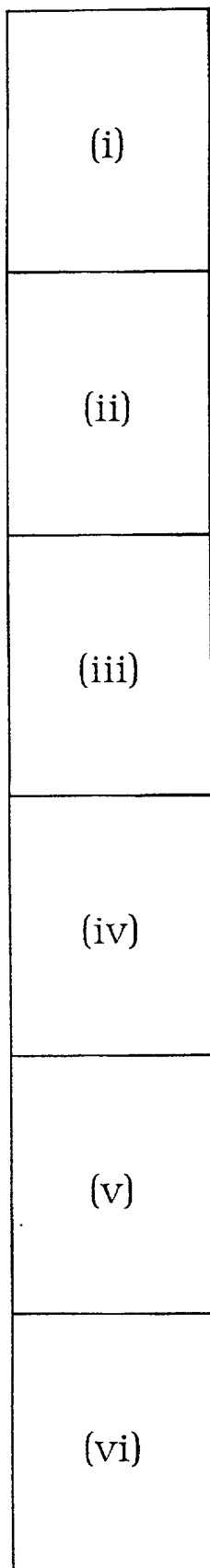


Figure 6

15/20

1 CAGGGCTGGG CGGCGGCGGC GGCGGCGGTC ATGGAACGCC AAGAGGAGTC
↑ transcription initiation site translation start codon
start exon 1
51 TCTGTCCGCG CGGCCGGCCC TGGAGACCGA GGGGCTGCGC TTCCTGCACA
101 CCACGGGTGA GTCGTTGCGG GGCAGCCGGG GCGCGCCGCG CACTTTTGCG
↑
end exon 1
151 ACGCGCAGCC ATGATGGGTG GGTCGTCCGC CGCTGCACCG GGCGCCGGAG
201 CCTGGGAGGC CTGGGAACGG TCGGGCGTTG GCGCTTACGC GGACCTTGGG
251 CAGCAGGCCC GGACCTTGCG CGGAGGCTTC TCGGGAGCCG CACTTCCCTG
301 GGCGGCTCGG CTGTCCCTTG TTTGCGCAAG TCTTTTTTGC GAACCAAGCC
351 CTTCTGTGG TAGTTACTGG GGTCACCTCG CCGTTGGCGT TTGCCTCTGG
401 GACCCGTCCC ACACAGCCCC ATACACACTC CTGACTCCCC GCGCTGTCAC
451 CCCTTTCTAT GTGGCTCTGA AAGGCCTTTG CCTTCCTGAT TCAGATTAGT
501 TGCTCTTCAT TCTTCAAAC CCAGTTGCTG TGCCCTCCAC ACTCTAACTG
551 CCCCCGACTC CCCAGATGGT TGGGAAGTCT CACTTCTCAG TGATCCCTGA
601 ATTGTCGCAC TTCTTGAGTT CGTGTTTTAA CGATCTACTT AGGAGGCTTT
651 TTCCTCAGCC TAGACCATGA AGGCTTTGAG GGCAGGAGTT AACTTTGTG
701 TTTGTTGAGT CTTATGGAAA GGTCAACTAG TAGTGTCATT TTTAGTTTTT
751 TGAAAACGTG TTTTCTTTTC AGTGGGCTCC CTGCTGGCCA CCTATGGCTG
↑
start exon 2
801 GTACATCGTC TTCAGCTGCA TCCTTCTCTA CGTGGTCTTT CAGAAGCTTT
851 CCGCCCGGCT AAGAGCCTTG AGGCAGAGGC AGCTGGACCG AGCTGCGGCT
901 GCTGTGGGTT AGTGCCTGAT AACCGAAATG AAAGCGGTGG TTTTGCACCT
↑
end exon 2

Figure 6(i)

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951 CCTTTATATT AAGAGTTAGT CTCTTAGTAA AAGTAAGAGG GGCCACACAG
1001 GAAGACCCTG TCTCTATTTA AAAAAAAAAA AAATAGCCGG GAGTGGCGGC
1051 ACGCACCTGT AGTCCCAGCT GCTCAGGAGG CTGAGGCGGG ATAATCACTT
1101 GAGTCCAGGG AGTCAAAGCT GCAGTGGGCT ATGCTCGGGC CACACTACAC
1151 TCCAGCCTGG GCAATTGATT GAGACCTTGT CTTTAAAAAA AAAAAAAAAA
1201 AAAAAGTAGG AAGTATATGG TTCTCGGTGG GCGCGGTGG CTCACACCTG
1251 TAATCCCAGC ACTTTGGGAA GCCGAGGCAG GAGGATGACT TGAGGTCAGG
1301 GGTTCGAGAA CAGCCTGGCC AACATGGTGA AACCCTGTCT CTAATAAAAA
1351 TACAAATATT AGTGGGGCGT GGTGACGGGC ACCTGTAATC CCAGCTATTA
1401 GGGTGGCTGA GGCAGGAGAA ATCGCTTGAA CCTGGGAGCT GGAGATTGCA
1451 GTGAGCTGAG ATTGTGCCAC TGCACTCCAG CCTGGGCAAC AGAGTGAGAC
1501 TGTCTTTTCT TTCTTTTTTT TTTTTTTTTC TATGAGATGG AGTCTAGCCT
1551 TGTTGCAAAG AGCGAGACTC TATGAGTAGA CGTTATGAAT AGAAATGAGT
1601 TCATTTCTAT TCATAATGCT ATTTGGAAGG ATTTTCTTT TCTGTAGAAA
1651 CAAATACTTA AGAATCTTCT GCGCTAATTA AGGGATGGAT AATGATTTAG
1701 AAAACTTTAT ATTCCTTGG TAGTCTTCCA GGATTCTAGT CAGCCTAGAG
1751 ACTGTGGGTG TCACTGAGGT ATCCAAGATG TGCTCTGTGT GGCCACTATC
1801 CCAGGCTTTA TGAATCGGAA TTGCTCAGGG GAACTCAGAA ATTGGCATT
1851 CTAACAGATT TCTGGTGATG TAGATATTTT GGGCTAAAAT CCGTGGCTCA
1901 GCAACAGACC CCTGCCCCCT GAAGCAGTAA AATGTATGCA GAGGGGTTAG
1951 GAGTACTTAT GTAAAAATAT GTTGTTTCAT TGTCTGATAT CCATACCTCT
2001 TTATACTTTT AATAATATGG AACTCAAAA GTTTCTATTT TATATTGTAC

Figure 6(ii)

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.55	0.50	0	1	-0.05	3.0	0.99
Marital Status	0.65	0.48	0	1	0.10	3.1	0.98
Education	12.5	2.5	9	16	-0.20	3.3	0.97
Income	15000	8000	5000	30000	0.30	3.4	0.96
Occupation	1.2	0.8	0	2	-0.10	3.0	0.99
Health Status	0.75	0.42	0	1	0.05	3.1	0.98
Stress Level	3.5	1.5	1	5	0.20	3.2	0.97
Life Satisfaction	4.2	1.2	1	5	-0.15	3.3	0.98
Resilience	2.8	1.0	1	4	0.10	3.1	0.98
Optimism	3.8	1.1	1	5	-0.10	3.2	0.98
Emotional Stability	3.2	1.0	1	5	0.05	3.1	0.98
Self-Esteem	3.5	1.1	1	5	-0.15	3.3	0.97
Life Purpose	3.0	1.2	1	5	0.10	3.2	0.98
Gratitude	3.8	1.0	1	5	-0.10	3.2	0.98
Forgiveness	3.5	1.1	1	5	0.05	3.1	0.98
Resilience	2.8	1.0	1	4	0.10	3.1	0.98
Optimism	3.8	1.1	1	5	-0.10	3.2	0.98
Emotional Stability	3.2	1.0	1	5	0.05	3.1	0.98
Self-Esteem	3.5	1.1	1	5	-0.15	3.3	0.97
Life Purpose	3.0	1.2	1	5	0.10	3.2	0.98
Gratitude	3.8	1.0	1	5	-0.10	3.2	0.98
Forgiveness	3.5	1.1	1	5	0.05	3.1	0.98

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.55	0.50	0	1	-0.05	3.0	0.99
Marital Status	0.65	0.48	0	1	0.10	3.1	0.98
Education	12.5	2.5	9	16	-0.20	3.3	0.97
Income	15000	8000	5000	30000	0.30	3.4	0.96
Occupation	1.2	0.8	0	2	-0.10	3.0	0.99
Health Status	0.75	0.42	0	1	0.05	3.1	0.98
Stress Level	3.5	1.5	1	5	0.20	3.2	0.97
Life Satisfaction	4.2	1.2	1	5	-0.15	3.3	0.98
Resilience	2.8	1.0	1	4	0.10	3.1	0.98
Optimism	3.8	1.1	1	5	-0.10	3.2	0.98
Emotional Stability	3.2	1.0	1	5	0.05	3.1	0.98
Self-Esteem	3.5	1.1	1	5	-0.15	3.3	0.97
Life Purpose	3.0	1.2	1	5	0.10	3.2	0.98
Gratitude	3.8	1.0	1	5	-0.10	3.2	0.98
Forgiveness	3.5	1.1	1	5	0.05	3.1	0.98
Empathy	3.2	1.0	1	5	-0.15	3.3	0.97
Resilience	2.8	1.0	1	4	0.10	3.1	0.98
Optimism	3.8	1.1	1	5	-0.10	3.2	0.98
Emotional Stability	3.2	1.0	1	5	0.05	3.1	0.98
Self-Esteem	3.5	1.1	1	5	-0.15	3.3	0.97
Life Purpose	3.0	1.2	1	5	0.10	3.2	0.98
Gratitude	3.8	1.0	1	5	-0.10	3.2	0.98
Forgiveness	3.5	1.1	1	5	0.05	3.1	0.98
Empathy	3.2	1.0	1	5	-0.15	3.3	0.97

SUBSTITUTE SHEET (RULE 26)RO/AU

18/20

2951 AGGAGGAAGA CAGTCCTGGG CCTTCCACTT CATCTGTCCT GAAACGGAAA
 ↑
 start exon 5

3001 TCGGACAGAA AGCCTTTGCG GGGAGGAGGT AAGCACCCTT GATGTCAAAT
 ↑
 end exon 5

3051 GTTAACAGAT TTTCAACACT TACAGGATAT AGTTACCTTT TAAGAACAAG
 3101 ATTGTTTGT TCTTTGTCCA TAAATTAAGA CTAATTCCTT AGGATTGTGA
 3151 AGATTCAATA AAGGAAACAG ATGCAAATCA CCTCCTAGGT CCTCACTAAG
 3201 TACTTAGAAG GATTGTACTT ATAGTATTCT AACTTGATCC TTCTGCAGCC
 3251 CCGTAGAGGG AGAGCTAAGT AGGGTGAGGA ATTGTCTGCC AATCTTCAGA
 3301 TGAGTGTCAA GGAGCTGGAA CACAGTGGTT TTGGTCTTTC TGGCTGGGAC
 3351 CACCTTGTTT CTTGCAAATA ACAAGGAGTA GCAGACAGAT GCTCATCCAA
 3401 AGCTGCTTCC TGTGTGCAGC ACTGCCCCGG GGAATCTGGA TGATGCCACA
 3451 GCAGTCTGTC TTCATCCCAT CCCTGAGAAT TTCAAATCTG GGAAGATGGG
 3501 ACTCACAAAC GAAAATAAGC AATCCTTGGT GATTCTGGCT AAGAGTTGCA
 3551 AGTTACTGCT GAGGAAGGAA AGAACAAACA CACTAGAACA CTGTAGGAAC
 3601 CAAGGCGGAA GATTTTGTAT CCTCCATAGG AGGAGAGGGG CACCGCAGAG
 3651 GCCCTGATGG TGTCTTTGAG GACTGAGGAA AGACTGGGGC ATGGGCTCCA
 3701 AGGCAGCAGG GCCACAGACT TGGCTGACCT TAAACGCTGA GCTGTAATCC
 3751 CCTTTGTGTC AGAAGACTAA ACCTGGCTTG CTGTAGAGAA GGTGATGCAT
 3801 CTGGAAAGAA AATGCTATTT TTAAATGGTC CTGCCGGAAG CTTATTTTTA
 3851 GACACATAGA GGTGATATTT AGGAGAGGAA TGGAAATCGT AGAAGATGGA
 3901 ATGCAGGGTG TGCTTGCCTG CACGGCCTCT TTCAGCATCC CCAGCATTTT
 3951 TGAGCTGGGA CTTTGTGACTA GCCTGGCTTT ACAAATAAGG AACTGAGGC

Figure 6(iv)

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4001 ACAGTGTTTA ATTGCCCAA GATTCCACTA TAAGTAAGGA GTAAAAGTAA
4051 CATTTAAGTT CTGGGTGGCC CTAGAACCTT AGCACTCAAC CAGGTTACCA
4101 GTTGTGCACT GACTTTGGGA AGCTCATGAG GGAGTGGGGT GGTGGGGGT
4151 AGGGAAGGAT ACAGAAGACC CCGTTCTGAC TGGTAGAAGT GACAAGTTTG
4201 ACTCTTGATT TTTTTTAATC TGTTTTCTGT AGCGTGAACA GCCCTTATTT
4251 GAATGTATGA GTTTTAGTAA GCACTGTGAT AGGAGGATTC ATATACTTAA
4301 ATCAGGCCCT CTTGAGAGAG TTTTTTGGTG ACCCTTTTGC ATGTGTTTCG
4351 GAGGTTGGGA CAAAGAAGCT GAATGACTTT TTTCCCCACC AGACAATCAG
4401 TTCAAATGGC AATCACAATA TAAAGGTTTT TTTTTTTTTC ACATAGCTAA
4451 AAGGTTTTTT TAAATGTCCC TTAGGATCTG TATCTTTGCA GTGCTTTGCG
4501 TGTCACCTCTC ATAATTTTAT TGTGGATATA CAATGTTCCC AGATTTTCAG
4551 ATTTTTATCA ATACTGTTGT GCTGCTTTTC TGTCCTCCCA GGTTATAACC
↑
start exon 6
4601 CGTTGTCTGG TGAAGGAGGC GGAGCTTGCT CCTGGAGACC TGGACGCAGA
4651 GGCCCGTCAT CTGGCGGATG AGGCTAAGAA TCTTGTTAGT GTCACTTTTG
↑
translation stop codon
4701 ACATTAGCAA GATGAACCCT TAACCCTCGA TTCAATTGCC TTACGCACGC
4751 TTTTCACAGT GACTAGCCAA GGGGAGGTGG GGTGATTTC TGTTCTAAC
4801 TACACCTGCA TATGTCAGGG CTCCAGTCAG CAAAAGGTAT AGATGTTGCC
4851 TCTAGGCATG AGGTCATTGG TCACATTCTA CTTGGAGACA GTGATTGCAT
4901 TCATTGATTT CATGGTTAAT TGCTAGTTGG TAGGTAAAGG CCTCTAGATG
4951 ATTAGCAATC TTGATAAAAG AGGCCTAGTA ATGTTCTTTT GAGGTTAGAA
5001 ATCCTTGCTG CTAGGACAGT CTCTGTGACA GGTGCGTTG AATGATGTCT

Figure 6(v)

SUBSTITUTE SHEET (RULE 26)RO/AU

20/20

5051 TCCTTATCAA TGGTGAGCCC ACCAGTGAGG ATTACTGATG TGGACAGTTG
5101 ATGGGGTTTG TTTCTGTATA TTTATTTTTA TGTACAGAAC TTTGTAAAAA
5151 CGAAACTATT TAAAAACAA GAATAACATT TTTAGCATCT TTATTCAAGG
5201 AGATTTATGG ACTTCAATTT GTCTATCAA CATTAAATAG CTTTTTATTA
5251 C
↑
transcription termination site
end exon 6

Figure 6(vi)